

[illegible]

(i) APPLICANT: Band, Vimla

(iii) NUMBER OF SEQUENCES: 11

(A) ADDRESSEE: Fish & Richardson P.C.

(C) CITY: Boston

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(A) MEDIUM TYPE: Floppy disk

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(A) APPLICATION NUMBER:

(B) FILING DATE:

(A) APPLICATION NUMBER: 08/467,155

(B) FILING DATE: 06-JUN-1995

(C) CLASSIFICATION:

(A) NAME: Clark, Paul T.

(B) REGISTRATION NUMBER: 30,162

(C) REFERENCE/DOCKET NUMBER: 00398/100002

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(C) TELEX: 200154

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala  
1 5 10 15

Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr  
35 40 45

Gly Ala Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val Ser Leu Phe  
50 55 60

Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp Gln Ser Trp  
65 70 75 80

Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp Ala Arg Val  
85 90 95

Gly Asp Asp His Leu Leu Leu Leu Gln Gly Glu Gln Leu Arg Arg Thr  
100 105 110

Thr Arg Ser Val Val His Pro Lys Tyr His Gln Gly Ser Gly Pro Ile  
115 120 125

Leu Pro Arg Arg Thr Asp Glu His Asp Leu Met Leu Leu Lys Leu Ala  
130 135 140

Arg Pro Val Val Pro Gly Pro Arg Val Arg Ala Leu Gln Leu Pro Tyr  
145 150 155 160

Arg Cys Ala Gln Pro Gly Asp Gln Cys Gln Val Ala Gly Trp Gly Thr  
165 170 175

Thr Ala Ala Arg Arg Val Lys Tyr Asn Lys Gly Leu Thr Cys Ser Ser  
180 185 190

Ile Thr Ile Leu Ser Pro Lys Glu Cys Glu Val Phe Tyr Pro Gly Val  
195 200 205

Val Thr Asn Asn Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro  
210 215 220

Cys Gln Ser Asp Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln  
225 230 235 240

Gly Ile Leu Ser Trp Gly Val Tyr Pro Cys Gly Ser Ala Gln His Pro  
245 250 255

Ala Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val  
260 265 270

Ile Arg Ser Asn  
275

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1454 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCCTCCCT CCTTCCTATC

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GGCGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC ACCTCTCCGC CGCCTCTGGC      120
GGCCGGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG      180
GCGCTGCTCC CCCAAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG      240
CGCGGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT      300
GTCCTGGTGG ACCAGAGTTG GGTGCTGACG GCCGCGCACT GCGGAAACAA GCCACTGTGG      360
GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCCG CCGGACGACT      420
CGCTCTGTTG TCCATCCCCA GTACCACCAG GGCTCAGGCC CCATCCTGCC AAGGCGAACG      480
GATGAGCAGC ATCTCATGTT GCTAAAGCTG GCCAGGCCCG TAGTGCCGGG GCCCCGCGTC      540
CGGGCCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGCTGGC      600
TGGGGCACCA CGGCCGCCCC GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCCAGCATC      660
ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCTG GCGTGGTCAC CAACAACATG      720
ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCCCTG      780
GTCTGTGACG AGACCCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC      840
CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA      900
CGCTCCAACT GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGCTGATC      960
CAGATGCCCCA GAGGCTCCAT CGTCCATCCT CTTCTCCCCC AGTCGGCTGA ACTCTCCCCT     1020
TGTCTGCACT GTTCAAACCT CTGCCGCCCT CCACACCTCT AAACATCTCC CCTCTCACCT     1080
CATTCCCCCA CCTATCCCCA TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG     1140
CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA     1200
CTGGGGTCAC CCAACCTGAC TTCCTCTGCC ACTCCCCGCT GTGTGACTTT GGGCAAGCCA     1260
AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG GGAACAATGA CGTGCCTACC     1320
TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT     1380
GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTTCCTGACT AAAGGTTACC TGTTGTCGTG     1440
AAAAAAAAAA AAAA                                                                1454

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCAGATTT AGGTGACAC

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCCTCTAAT ACGACTCAC

19

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TACCACTACA ATGGATG

17

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTGAAGTGA ACTTGCGGGC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

TOCTCT "BSET2001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Phe  
1 5 10 15  
Pro Val Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Met Met Thr Arg  
20 25 30  
Tyr Ala Arg Thr Cys Arg Glu Ser Ser Val Pro Tyr Gln Val Ser Leu  
35 40 45  
Asn Ala Gly Tyr His Phe Cys Gly Gly Ser Leu Ile Asn Asp Gln Trp  
50 55 60  
Val Val Ser Ala Ala His Cys Tyr Lys Tyr Arg Ile Gln Val Arg Leu  
65 70 75 80  
Gly Glu His Asn Met Met Thr Arg Tyr Ala Arg Ile Asn Val Leu Glu  
85 90 95  
Gly Asn Glu Gln Phe Val Asp Ser Ala Lys Ile Ile Arg His Pro Asn  
100 105 110  
Tyr Asn Ser Trp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys Leu Ala  
115 120 125  
Ser Pro Val Thr Leu Met Met Thr Arg Tyr Ala Arg Asn Ala Arg Val  
130 135 140  
Ala Ser Val Pro Leu Pro Ser Ser Cys Ala Pro Ala Gly Thr Gln Cys  
145 150 155 160  
Leu Ile Ser Gly Trp Gly Asn Thr Leu Ser Asn Gly Val Asn Asn Pro  
165 170 175  
Asp Leu Leu Gln Cys Val Asp Ala Pro Val Leu Pro Gln Ala Met Met  
180 185 190  
Thr Arg Tyr Ala Arg Asp Cys Glu Ala Ser Tyr Pro Gly Asp Ile Thr  
195 200 205  
Asn Asn Met Ile Cys Val Gly Phe Leu Glu Gly Gly Lys Asp Ser Cys  
210 215 220  
Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Glu Leu Gln Gly  
225 230 235 240  
Ile Val Ser Trp Gly Tyr Met Met Thr Arg Tyr Ala Arg Gly Cys Ala  
245 250 255  
Gln Pro Asp Ala Pro Gly Val Tyr Thr Lys Val Cys Asn Tyr Val Asp  
260 265 270  
Trp Ile Gln Asn Thr Ile Ala Asp Asn  
275 280

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Glu Leu His Pro Leu Leu Gly Gly Arg Thr Trp Arg Ala Ala Arg  
1 5 10 15  
Asp Ala Asp Gly Cys Glu Ala Leu Gly Thr Val Ala Val Pro Phe Asp  
20 25 30  
Asp Asp Asp Lys Ile Val Gly Gly Tyr His Ser Thr Arg Tyr Ile Val  
35 40 45  
Asx Thr Cys Glu Asn Ser Leu Pro Tyr Gln Val Ser Leu Asn Ser Gly  
50 55 60  
Ser His Phe Cys Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser  
65 70 75 80  
Ala Ala His Cys Tyr Lys Thr Arg Ile Gln Val Arg Leu Gly Glu His  
85 90 95  
Asn His Ser Thr Arg Tyr Ile Val Asx Ile Lys Val Leu Glu Gly Asn  
100 105 110  
Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro Lys Tyr Asn  
115 120 125  
Arg Asp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys Leu Ser Ser Pro  
130 135 140  
Ala Val Ile His Ser Thr Arg Tyr Ile Val Asx Asn Ala Arg Val Ser  
145 150 155 160  
Thr Ile Ser Leu Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Cys Leu  
165 170 175  
Ile Ser Gly Trp Gly Asn Thr Leu Ser Phe Gly Ala Asp Tyr Pro Asp  
180 185 190  
Glu Leu Lys Cys Leu Asp Ala Pro Val Leu Thr Gln Ala His Ser Thr  
195 200 205  
Arg Tyr Ile Val Asx Glu Cys Lys Ala Ser Tyr Pro Gly Lys Ile Thr  
210 215 220  
Asn Ser Met Phe Cys Val Gly Phe Leu Glu Gly Gly Lys Asp Ser Cys  
225 230 235 240  
Gln Arg Asp Ser Gly Gly Pro Val Val Cys Asn Gly Gln Leu Gln Gly  
245 250 255  
Val Val Ser Trp Gly His His Ser Thr Arg Tyr Ile Val Asx Gly Cys  
260 265 270  
Ala Trp Lys Asn Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val  
275 280 285  
Asp Trp Ile Lys Asp Thr Ile Ala Ala Asn Ser  
290 295

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Lys Ile Cys Ile Phe Phe Thr Leu Leu Gly Thr Val Ala Ala Phe  
1 5 10 15  
Pro Thr Glu Asp Asn Asp Asp Arg Ile Val Gly Gly Tyr Arg Asn Thr  
20 25 30  
Arg Tyr Pro Val Asx Thr Cys Gln Glu His Ser Val Pro Tyr Gln Val  
35 40 45  
Ser Leu Asn Ala Gly Ser His Ile Cys Gly Gly Ser Leu Ile Thr Asp  
50 55 60  
Gln Trp Val Leu Ser Ala Ala His Cys Tyr His Pro Gln Leu Gln Val  
65 70 75 80  
Arg Leu Gly Glu His Asn Arg Asn Thr Arg Tyr Pro Val Asx Ile Tyr  
85 90 95  
Glu Ile Glu Gly Ala Glu Gln Phe Ile Asp Ala Ala Lys Met Ile Leu  
100 105 110  
His Pro Asp Tyr Asp Lys Trp Thr Val Asp Asn Asp Ile Met Leu Ile  
115 120 125  
Lys Leu Lys Ser Pro Ala Thr Leu Arg Asn Thr Arg Tyr Pro Val Asx  
130 135 140  
Asn Ser Lys Val Ser Thr Ile Pro Leu Pro Gln Tyr Cys Pro Thr Ala  
145 150 155 160  
Gly Thr Glu Cys Leu Val Ser Gly Trp Gly Val Leu Lys Phe Gly Phe  
165 170 175  
Glu Ser Pro Ser Val Leu Gln Cys Leu Asp Ala Pro Val Leu Ser Asp  
180 185 190  
Ser Arg Asn Thr Arg Tyr Pro Val Asx Val Cys His Lys Ala Tyr Pro  
195 200 205  
Arg Gln Ile Thr Asn Asn Met Phe Cys Leu Gly Phe Leu Glu Gly Gly  
210 215 220  
Lys Asp Ser Cys Gln Tyr Asp Ser Gly Gly Pro Val Val Cys Asn Gly  
225 230 235 240  
Glu Val Gln Gly Ile Val Ser Trp Gly Asp Arg Asn Thr Arg Tyr Pro  
245 250 255

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INFORMATION FOR SEQ ID NO:10:

(A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Ala | Phe | Ala | Thr | Glu | Asp | Asp | Lys | Ile | Val | Gly | Gly | Tyr | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Arg | Tyr | Pro | Ile | Ile | Glu | Cys | Lys | Ala | Tyr | Ser | Gln | Pro | His | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ser | Leu | Asn | Ser | Gly | Tyr | His | Phe | Cys | Gly | Gly | Ser | Leu | Val | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Asn | Trp | Val | Val | Ser | Ala | Ala | His | Cys | Tyr | Gln | Ser | Arg | Val | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Arg | Leu | Gly | Glu | His | Asn | Ser | Ser | Thr | Arg | Tyr | Pro | Ile | Ile | Ile |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gln | Val | Thr | Glu | Gly | Ser | Glu | Gln | Phe | Ile | Ser | Ser | Ser | Arg | Val | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | His | Pro | Asn | Tyr | Ser | Ser | Tyr | Asn | Ile | Asp | Asn | Asp | Ile | Met | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Lys | Leu | Ser | Lys | Pro | Ala | Thr | Leu | Ser | Ser | Thr | Arg | Tyr | Pro | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Asn | Thr | Tyr | Val | Gln | Pro | Val | Ala | Leu | Pro | Thr | Ser | Cys | Ala | Pro |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Gly | Thr | Met | Cys | Thr | Val | Ser | Gly | Trp | Gly | Asn | Thr | Met | Ser | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Ala | Asp | Lys | Asn | Lys | Leu | Gln | Cys | Leu | Asn | Ile | Pro | Ile | Leu | Ser |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Tyr | Ser | Ser | Ser | Thr | Arg | Tyr | Pro | Ile | Ile | Asp | Cys | Asn | Asn | Ser | Tyr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Pro | Gly | Met | Ile | Thr | Asn | Ala | Met | Phe | Cys | Ala | Gly | Tyr | Leu | Glu | Gly |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gly | Lys | Asp | Ser | Cys | Gln | Gly | Asp | Ser | Gly | Gly | Pro | Val | Val | Cys | Asn |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |



Gly Glu Leu Gln Gly Val Val Ser Trp Gly Tyr Ser Ser Thr Arg Tyr  
 225 230 235 240  
 Pro Ile Ile Gly Cys Ala Glu Pro Gly Asn Pro Gly Val Tyr Ala Lys  
 245 250 255  
 Val Cys Ile Phe Asn Asp Trp Leu Thr Ser Thr Met Ala Thr Tyr  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala  
 1 5 10 15  
 Leu Ala Lys Leu Leu Pro Leu Leu Met Ala Gln Leu Trp Ala Ala Glu  
 20 25 30  
 Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr  
 35 40 45  
 Gly Ala Asn Glu Ser Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val  
 50 55 60  
 Ser Leu Phe Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp  
 65 70 75 80  
 Gln Ser Trp Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp  
 85 90 95  
 Ala Arg Val Gly Asp Asp His Asn Glu Ser Leu Leu Leu Leu Gln Gly  
 100 105 110  
 Glu Gln Leu Arg Arg Thr Thr Arg Ser Val Val His Pro Lys Tyr His  
 115 120 125  
 Gln Gly Ser Gly Pro Ile Leu Pro Arg Arg Thr Asp Glu His Asp Leu  
 130 135 140  
 Met Leu Leu Lys Leu Ala Arg Pro Val Val Pro Asn Glu Ser Gly Pro  
 145 150 155 160  
 Arg Val Arg Ala Leu Gln Leu Pro Tyr Arg Cys Ala Gln Pro Gly Asp  
 165 170 175  
 Gln Cys Gln Val Ala Gly Trp Gly Thr Thr Ala Ala Arg Arg Val Lys  
 180 185 190  
 Tyr Asn Lys Gly Leu Thr Cys Ser Ile Thr Ile Leu Ser Pro Lys  
 195 200 205

1003360-12201

Asn Glu Ser Glu Cys Glu Val Phe Tyr Pro Gly Val Val Thr Asn Asn  
210 215 220

Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro Cys Gln Ser Asp  
225 230 235 240

Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln Gly Ile Leu Ser  
245 250 255

Trp Gly Val Tyr Asn Glu Ser Pro Cys Gly Ser Ala Gln His Pro Ala  
260 265 270

Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val Ile  
275 280 285

Arg Ser Asn  
290

FOOTNOTES: 11001